



Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

Structure

seq 33

seq 23

BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.17 [Aug-26-2007]

Match: Mismatch: gap open: gap extension: x_dropoff: expect: wordsize: Filter ☐ View option Masking character option ☒ X for protein, n for nucleotide Masking color option ☐ Show CDS translation

Sequence 1: lcl|1

Length = 529 (1 .. 529)

Sequence 2: lcl|65536

Length = 1895 (1 .. 1895)

Instant seq ID NO: 33

Instant seq ID NO: 23

Alignment 1
part of Paper No: 20080103



NOTE: Bitscore and expect value are calculated based on the size of the nr database.

NOTE: If protein translation is reversed, please repeat the search with reverse strand of the query sequence.

Score = 1017 bits (529), Expect = 0.0
Identities = 529/529 (100%), Gaps = 0/529 (0%)
Strand=Plus/Minus

Query	1	TTTGGTTTCTCCAGTAGGAGTTCTCATCATATATTTTCATTCATTTTCATCTATTTCTGCTGGG	60
Sbjct	982	TTTGGTTTCTCCAGTAGGAGTTCTCATCATATATTTTCATTCATTTTCATCTATTTCTGCTGGG	923
Query	61	CTGATCGAATGAGCTCCTGGATGTTCTCCATTATCATAGGAGTAGACTCTACTTCTCGTA	120
Sbjct	922	CTGATCGAATGAGCTCCTGGATGTTCTCCATTATCATAGGAGTAGACTCTACTTCTCGTA	863
Query	121	CCCGGGGAGCAAAAGAGGAAGGGTTAGAAGATAGAGATTGAGAGTGAAACTTGGGCTCTG	180

```
Sbjct  862  CCCGGGGAGCAAAGAGGAAGGGTTAGAAGATAGAGATTCAGAGTGAAACTTGGGCTCTG  803
Query  181  AGTCTGTCTGCAGCTGAGACACAGCCTCCCGTCCCTCCTTAGTCCCCTGTCCTTCTTCCT  240
          |||
Sbjct  802  AGTCTGTCTGCAGCTGAGACACAGCCTCCCGTCCCTCCTTAGTCCCCTGTCCTTCTTCCT  743
Query  241  GCTTTCCTCCTCTTCTCTGTTCTCTTCTTGCTCTTCCTGTTTCTGCCCCTCTTCCTGCT  300
          |||
Sbjct  742  GCTTTCCTCCTCTTCTCTGTTCTCTTCTTGCTCTTCCTGTTTCTGCCCCTCTTCCTGCT  683
Query  301  TGTGTTCTTGTGTGCGGCTCCTGCCTGTGCTCCACTCCTTGCTCCTGCTTGTGCTCTGGCG  360
          |||
Sbjct  682  TGTGTTCTTGTGTGCGGCTCCTGCCTGTGCTCCACTCCTTGCTCCTGCTTGTGCTCTGGCG  623
Query  361  CTTGCTCCTGGCCTCCCAGGGACAAGGAGGATTGTAGGAGCTCTTCCACGTTGTTGCTGA  420
          |||
Sbjct  622  CTTGCTCCTGGCCTCCCAGGGACAAGGAGGATTGTAGGAGCTCTTCCACGTTGTTGCTGA  563
Query  421  GCCTCTCAGGCCAGGGCTGGAAGGTCTGGCGTTCTGTCACTGTGAAGTGGGGTGAGATGG  480
          |||
Sbjct  562  GCCTCTCAGGCCAGGGCTGGAAGGTCTGGCGTTCTGTCACTGTGAAGTGGGGTGAGATGG  503
Query  481  GGGAGGTCATCGTGGTGGGTGAGACTTCAGCTGAAGCTTCTATCTCCTT  529
          |||
Sbjct  502  GGGAGGTCATCGTGGTGGGTGAGACTTCAGCTGAAGCTTCTATCTCCTT  454
```

CPU time: 0.05 user secs. 0.03 sys. secs 0.08 total secs.



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 Match: Mismatch: gap open: gap extension:

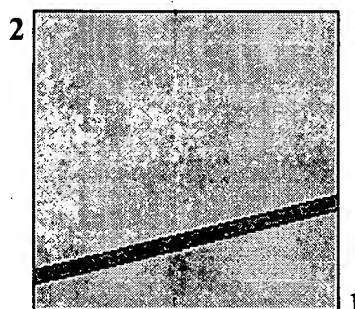
 x_dropoff: expect: wordsize: Filter ☒ View option

 Masking character option Masking color option
☐ Show CDS translation
Sequence 1: lcl|1

Length = 460 (1 .. 460)

Sequence 2: lcl|65536

Length = 1895 (1 .. 1895)

Jacobs Seg Id 11
Instant Seg Id 23

*Alignment 2
part of Paper No. 2008 0103*

NOTE: Bitscore and expect value are calculated based on the size of the nr database.

NOTE: If protein translation is reversed, please repeat the search with reverse strand of the query sequence.

 Score = 885 bits (460), Expect = 0.0
 Identities = 460/460 (100%), Gaps = 0/460 (0%)
 Strand=Plus/Plus

Query	1	GCCGTCTCCGTGCAACCCACGGCTGCCGGAATCCCACACTCGTCCAGCTGGACCAATATG	60
Sbjct	227	GCCGTCTCCGTGCAACCCACGGCTGCCGGAATCCCACACTCGTCCAGCTGGACCAATATG	286
Query	61	AAAACCACGGCTTAGTGCCCGATGGTGCTGTCTGCTCCAACCTCCCTTATGCCTCCTGGT	120
Sbjct	287	AAAACCACGGCTTAGTGCCCGATGGTGCTGTCTGCTCCAACCTCCCTTATGCCTCCTGGT	346
Query	121	TTGAGTCTTTCTGCCAGTTCACCTCACTACCGTTGCTCCAACCACGTCTACTATGCCAAGA	180

```
Sbjct  347  TTGAGTCTTTCTGCCAGTTCACCTCACTACCGTTGCTCCAACCACGTCTACTATGCCAAGA  406
Query  181  GAGTCCTGTGTTCCCAGCCAGTCTCTATTCTCTCACCTAACACTCTCAAGGAGATAGAAG  240
          |||
Sbjct  407  GAGTCCTGTGTTCCCAGCCAGTCTCTATTCTCTCACCTAACACTCTCAAGGAGATAGAAG  466
Query  241  CTTCAGCTGAAGTCTCACCCACCACGATGACCTCCCCCATCTCACCCCACTTCACAGTGA  300
          |||
Sbjct  467  CTTCAGCTGAAGTCTCACCCACCACGATGACCTCCCCCATCTCACCCCACTTCACAGTGA  526
Query  301  CAGAACGCCAGACCTTCCAGCCCTGGCCTGAGAGGCTCAGCAACAACGTGGAAGAGCTCC  360
          |||
Sbjct  527  CAGAACGCCAGACCTTCCAGCCCTGGCCTGAGAGGCTCAGCAACAACGTGGAAGAGCTCC  586
Query  361  TACAATCCTCCTTGTCCCTGGGAGGCCAGGAGCAAGCGCCAGAGCACAAAGCAGGAGCAAG  420
          |||
Sbjct  587  TACAATCCTCCTTGTCCCTGGGAGGCCAGGAGCAAGCGCCAGAGCACAAAGCAGGAGCAAG  646
Query  421  GAGTGGAGCACAGGCAGGAGCCGACACAAGAACAACAAGCA  460
          |||
Sbjct  647  GAGTGGAGCACAGGCAGGAGCCGACACAAGAACAACAAGCA  686
```

CPU time: 0.03 user secs. 0.03 sys. secs 0.06 total secs.



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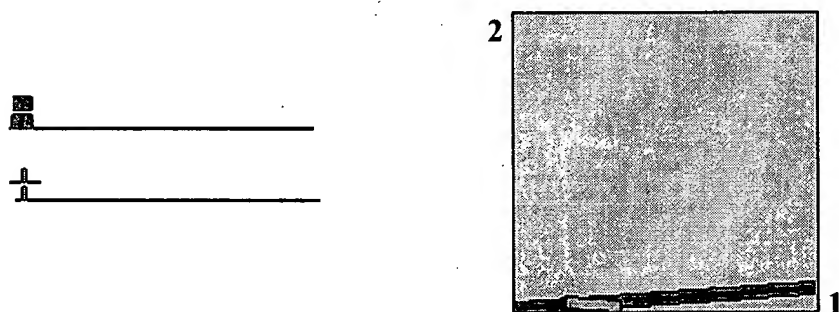
BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.17 [Aug-26-2007]

Match: Mismatch: gap open: gap extension: x_dropoff: expect: wordsize: Filter ☐ View option Masking character option Masking color option ☐ Show CDS translation **Sequence 1:** gi|22619253|5'EST of secreted protein expressing in testis and other tissues

Length = 128 (1 .. 128)

Sequence 2: lcl|65536

Length = 1895 (1 .. 1895)

*Dumas milne Edwards SEQ ID NO:60**Instant SEQ ID NO:23*

*Alignment 3
part of Paper No. 20080103*

NOTE: Bitscore and expect value are calculated based on the size of the nr database.

NOTE: If protein translation is reversed, please repeat the search with reverse strand of the query sequence.



Score = 237 bits (123), Expect = 9e-60
Identities = 125/126 (99%), Gaps = 0/126 (0%)
Strand=Plus/Plus

```

Query 2      GGGCGGATCTTCTCCGGCCATGAGGAAGCCAGCCGCTGGCTTCCTTCCCTCACTCCTGAA 61
            |||
Sbjct 30      GGGCGGATCTTCTCCGGCCATGAGGAAGCCAGCCGCTGGCTTCCTTCCCTCACTCCTGAA 89

Query 62      GGTGCTGCTCCTGCCTCTGGCACCTGCCGAGCCAGGATTCGACTCAGGCCTCCACTCC 121
            |||
Sbjct 90      GGTGCTGCTCCTGCCTCTGGCACCTGCCGAGCCAGGATTCGACTCAGGCCCCCACTCC 149

Query 122     AGGCAG 127
            |||||

```

Sbjct 150 AGGCAG 155



Score = 39.1 bits (20), Expect = 3.9
Identities = 22/23 (95%), Gaps = 0/23 (0%)
Strand=Plus/Minus

Query 24 AGGAAGCCAGCCGCTGGCTTCCT 46
 ||||| |||||
Sbjct 74 AGGAAGCCAGCGGCTGGCTTCCT 52

CPU time: 0.05 user secs. 0.05 sys. secs 0.10 total secs.